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INPUT SET: S23737.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                                        SEQUENCE LISTING      ENTERED
 2
 3    (1)    General Information:
 4
 5       (i) APPLICANT:   Marc F. Charette
 6
 7      (ii) TITLE OF INVENTION: Methods and Compositions for   Enhancing Cognitive Func
 8
 9     (iii) NUMBER OF SEQUENCES: 9
10
11     (iv) CORRESPONDENCE ADDRESS:
12             (A) ADDRESSEE: CREATIVE BIOMOLECULES, INC
13             (B) STREET: 45 SOUTH STREET
14             (C) CITY: HOPKINTON
15             (D) STATE: MA
16             (E) COUNTRY: USA
17             (F) ZIP: 01748
18
19      (v) COMPUTER READABLE FORM:
20             (A) MEDIUM TYPE: Floppy disk
21             (B) COMPUTER: IBM PC compatible
22             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25     (vi) CURRENT APPLICATION DATA:
26             (A) APPLICATION NUMBER:
27             (B) FILING DATE:
28             (C) CLASSIFICATION:
29
30   (viii) ATTORNEY/AGENT INFORMATION:
31             (A) NAME: Thomas C. Meyers
32             (B) REGISTRATION NUMBER:
33             (C) REFERENCE/DOCKET NUMBER: CRP-141
34
35     (ix) TELECOMMUNICATION INFORMATION:
36             (A) TELEPHONE: (617) 248-7000
37             (B) TELEFAX: (617) 248-7100
38
39
40   (2) INFORMATION FOR SEQ ID NO:1:
41
42      (i) SEQUENCE CHARACTERISTICS:
43             (A) LENGTH: 1822 base pairs
44             (B) TYPE: nucleic acid
45             (C) STRANDEDNESS: single
46             (D) TOPOLOGY: linear
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INPUT SET: S23737.raw

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47
48        (ii) MOLECULE TYPE: cDNA
49
50        (vi) ORIGINAL SOURCE:
51              (A) ORGANISM: HOMO SAPIENS
52              (F) TISSUE TYPE: HIPPOCAMPUS
53
54        (ix) FEATURE:
55              (A) NAME/KEY: CDS
56              (B) LOCATION: 49..1341
57              (C) IDENTIFICATION METHOD: experimental
58              (D) OTHER INFORMATION: /function= "MORPHOGENIC PROTEIN"
59     /product= "OP1"
60     /evidence= EXPERIMENTAL
61     /standard_name= "OP1"
62
63
64        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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66     GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG        57
67                                                          Met His Val
68                                                           1
69
70     CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA       105
71     Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
72          5                   10                  15
73
74     CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC       153
75     Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
76      20                  25                  30                  35
77
78     GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG       201
79     Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
80                  40                  45                  50
81
82     CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC       249
83     Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
84                  55                  60                  65
85
86     CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG       297
87     Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
88              70                  75                  80
89
90     CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC       345
91     Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
92          85                  90                  95
93
94     GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC       393
95     Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
96     100                 105                 110                 115
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98     CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC       441
99     Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
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INPUT SET: S23737.raw

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104                135                      140                      145
105
106   CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC      537
107   His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
108                150                      155                      160
109
110   CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC      585
111   Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
112          165                      170                      175
113
114   TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT      633
115   Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
116   180                      185                      190                      195
117
118   CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC      681
119   Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
120                200                      205                      210
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122   GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC      729
123   Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
124                215                      220                      225
125
126   ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG      777
127   Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
128                230                      235                      240
129
130   GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC      825
131   Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
132          245                      250                      255
133
134   AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC      873
135   Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
136   260                      265                      270                      275
137
138   TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC      921
139   Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
140                280                      285                      290
141
142   CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC      969
143   Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
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145
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147   Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
148                310                      315                      320
149
150   AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC      1065
151   Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
152          325                      330                      335
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INPUT SET: S23737.raw

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153
154     CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC     1113
155     Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
156     340             345             350             355
157
158     GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG     1161
159     Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
160             360             365             370
161
162     AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC     1209
163     Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
164             375             380             385
165
166     CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC     1257
167     Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
168             390             395             400
169
170     ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA     1305
171     Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
172         405             410             415
173
174     TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC          1351
175     Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
176     420             425             430
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178     GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG   1411
179
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182     TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC   1531
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184     ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC   1591
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186     GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT   1651
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188     CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG   1711
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190     GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC   1771
191
192     CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAA A              1822
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195     (2) INFORMATION FOR SEQ ID NO:2:
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197             (i) SEQUENCE CHARACTERISTICS:
198                 (A) LENGTH: 431 amino acids
199                 (B) TYPE: amino acid
200                 (D) TOPOLOGY: linear
201
202             (ii) MOLECULE TYPE: protein
203
204             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
205
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/012,846*

INPUT SET: S23737.raw

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210                20                  25              30
211
212   Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
213            35              40                  45
214
215   Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
216        50              55                  60
217
218   Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
219    65              70                  75                  80
220
221   Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
222                85                  90                  95
223
224   Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
225                100                 105                 110
226
227   Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
228                115                 120                 125
229
230   Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
231        130             135                 140
232
233   Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
234   145             150                 155                 160
235
236   Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
237                165                 170                 175
238
239   Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
240                180                 185                 190
241
242   Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
243        195                 200                 205
244
245   Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
246        210                 215                 220
247
248   Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
249   225             230                 235                 240
250
251   His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
252                245                 250                 255
253
254   Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
255                260                 265                 270
256
257   Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/012,846*

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